

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0256 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Consensus

(B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Ala	Ser	Ala	Arg	Leu	Leu	Arg	Ala	Val	Ile	Met	Gly	Ala	Pro
1				5					10					15	
Gly	Ser	Gly	Lys	Gly	Thr	Val	Ser	Ser	Arg	Ile	Thr	Thr	His	Phe	Glu
			20					25					30		
Leu	Lys	His	Leu	Ser	Ser	Gly	Asp	Leu	Leu	Arg	Asp	Asn	Met	Leu	Arg
		35					40					45			
Gly	Thr	Glu	Ile	Gly	Val	Leu	Ala	Lys	Ala	Phe	Ile	Asp	Gln	Gly	Lys
	50					55					60				
Leu	Ile	Pro	Asp	Asp	Val	Met	Thr	Arg	Leu	Ala	Leu	His	Glu	Leu	Lys
65					70					75					80
Asn	Leu	Thr	Gln	Tyr	Ser	Trp	Leu	Leu	Asp	Gly	Phe	Pro	Arg	Thr	Leu
			85						90					95	
Pro	Gln	Ala	Glu	Ala	Leu	Asp	Arg	Ala	Tyr	Gln	Ile	Asp	Thr	Val	Ile
			100					105					110		
Asn	Leu	Asn	Val	Pro	Phe	Glu	Val	Ile	Lys	Gln	Arg	Leu	Thr	Ala	Arg
	115						120						125		
Trp	Ile	His	Pro	Ala	Ser	Gly	Arg	Val	Tyr	Asn	Ile	Glu	Phe	Asn	Pro
	130					135					140				
Pro	Lys	Thr	Val	Gly	Ile	Asp	Asp	Leu	Thr	Gly	Glu	Pro	Leu	Ile	Gln
145					150					155					160
Arg	Glu	Asp	Asp	Lys	Pro	Glu	Thr	Val	Ile	Lys	Arg	Leu	Lys	Ala	Tyr
				165					170					175	
Glu	Asp	Gln	Thr	Lys	Xaa	Val	Leu	Xaa	Tyr	Tyr	Gln	Lys	Lys	Gly	Val
			180					185					190		
Leu	Glu	Thr	Phe	Ser	Gly	Thr	Glu	Thr	Asn	Lys	Ile	Trp	Pro	Tyr	Val
	195						200					205			
Tyr	Ala	Phe	Leu	Gln	Thr	Lys	Val	Pro	Gln	Arg	Ser	Gln	Lys	Ala	Ser
	210					215					220				
Val	Thr	Pro													
225															

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Consensus

(B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCANGCCCA	AAGCCCTGGT	ACCCGCGCGG	TGGGGCCTCA	GTCTGCGGCC	ATGGGGGCGT	60
CCGCGCGGCT	GCTGCGAGCG	GTGATCATGG	GGGCCCCGGG	CTCGGGCAAG	GGCACCGTGT	120
CGTCGCGCAT	CACTACACAC	TTTCGAGCTGA	AGCACCTCTC	CAGCGGGGAC	CTGCTCCGGG	180

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ACAACATGCT GCGGGGCACA GAAATTGGCG TGTTAGCCAA GGCTTTCATT GACCAAGGGA 240
AACTCATCCC AGATGATGTC ATGACTCGGC TGGCCCTTCA TGAGCTGAAA AATCTCACCC 300
AGTATAGCTG GCTGTTGGAT GGTTTTCCAA GGACACTTCC ACAGGCAGAA GCCCTAGATA 360
GAGCTTATCA GATCGACACA GTGATTAACC TGAATGTGCC CTTTGAGGTC ATTAAACAAC 420
GCCTTACTGC TCGCTGGATT CATCCCGCCA GTGGCCGAGT CTATAACATT GAATTCAACC 480
CTCCCAAAAC TGTGGGCATT GATGACCTGA CTGGGGAGCC TCTCATTAG CGTGAGGATG 540
ATAAACCAGA GACGGTTATC AAGAGACTAA AGGCTTATGA AGACCAAACA AAGNCAGTCC 600
TGGNATATTA CCAGAAAAAA GGGGTGCTGG AAACATTCTC CGGAACAGAA ACCAACAAGA 660
TTTGGCCCTA TGATATGCT TTCCTACAAA CTAAAGTTCC ACAAAGAAGC CAGAAAGCTT 720
CAGTTACTCC ATGAGGAGAA ATGTGTGTAA CTATTAATAG TAAGATGGGC AAACCTCCTA 780
GTCCTTGCAT TTAGAAGCTG CTTTTCCTAA GACTTCTAGT ATGTATGAAT TCTTTGAAAA 840
TTATATTACT TTTA 854

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 217576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Ala Ile Met Gly Ala Pro
1          5          10          15
Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Lys His Phe Glu
20          25          30
Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
35          40          45
Gly Thr Glu Ile Gly Val Leu Ala Lys Thr Phe Ile Asp Gln Gly Lys
50          55          60
Leu Ile Pro Asp Asp Val Met Thr Arg Leu Val Leu His Glu Leu Lys
65          70          75          80
Asn Leu Thr Gln Tyr Asn Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
85          90          95
Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
100         105         110
Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
115         120         125
Trp Ile His Pro Gly Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
130         135         140
Pro Lys Thr Met Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Val Gln
145         150         155         160
Arg Glu Asp Asp Arg Pro Glu Thr Val Val Lys Arg Leu Lys Ala Tyr
165         170         175
Glu Ala Gln Thr Glu Pro Val Leu Glu Tyr Tyr Arg Lys Lys Gly Val
180         185         190
Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro His Val
195         200         205
Tyr Ala Phe Leu Gln Thr Lys Leu Pro Gln Arg Ser Gln Glu Thr Ser

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210
Val Thr Pro
225

215

220

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 450312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Ser Gly Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
1 5 10 15
Gly Ser Gly Lys Gly Thr Gly Ser Ser Arg Ile Thr Lys His Phe Glu
20 25 30
Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Gln Asn Met Leu Gln
35 40 45
Gly Thr Glu Ile Ala Val Leu Ala Lys Ser Phe Ile Asp Gln Gly Lys
50 55 60
Leu Ile Pro Asp Asp Asp Met Thr Arg Leu Ala Leu His Glu Leu Lys
65 70 75 80
Asn Leu Thr Gln Cys Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
85 90 95
Pro Gln Ala Glu Ala Leu Asp Arg Val Tyr Gln Ile Asp Thr Val Ile
100 105 110
Asn Leu Asn Val Pro Phe Glu Val Ile Lys Leu Arg Leu Thr Ala Arg
115 120 125
Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
130 135 140
Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
145 150 155 160
Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
165 170 175
Glu Ala Gln Thr Glu Pro Val Leu Gln Tyr Tyr Gln Lys Lys Gly Val
180 185 190
Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Arg Pro His Val
195 200 205
Tyr Ser Phe Leu Gln Met Lys Val Pro Glu Thr Ile Gln Lys Ala Ser
210 215 220
Val Thr Pro
225

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 28577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Ser	Lys	Leu	Leu	Arg	Ala	Val	Ile	Leu	Gly	Pro	Pro	Gly	Ser
1				5					10					15	
Gly	Lys	Gly	Thr	Val	Cys	Gln	Arg	Ile	Ala	Gln	Asn	Phe	Gly	Leu	Gln
			20					25					30		
His	Leu	Ser	Ser	Gly	His	Phe	Leu	Arg	Glu	Asn	Ile	Lys	Ala	Ser	Thr
		35					40					45			
Glu	Val	Gly	Glu	Met	Ala	Lys	Gln	Tyr	Ile	Glu	Lys	Ser	Leu	Leu	Val
	50					55					60				
Pro	Asp	His	Val	Ile	Thr	Arg	Leu	Met	Met	Ser	Glu	Leu	Glu	Asn	Arg
65					70					75				80	
Arg	Gly	Gln	His	Trp	Leu	Leu	Asp	Gly	Phe	Pro	Arg	Thr	Leu	Gly	Gln
				85					90					95	
Ala	Glu	Ala	Leu	Asp	Lys	Ile	Cys	Glu	Val	Asp	Leu	Val	Ile	Ser	Leu
			100					105					110		
Asn	Ile	Pro	Phe	Glu	Thr	Leu	Lys	Asp	Arg	Leu	Ser	Arg	Arg	Trp	Ile
		115					120					125			
His	Pro	Pro	Ser	Gly	Arg	Val	Tyr	Asn	Leu	Asp	Phe	Asn	Pro	Pro	His
		130				135					140				
Val	His	Gly	Ile	Asp	Asp	Val	Thr	Gly	Glu	Pro	Leu	Val	Gln	Gln	Glu
145					150					155					160
Asp	Asp	Lys	Pro	Glu	Ala	Val	Ala	Ala	Arg	Leu	Arg	Gln	Tyr	Lys	Asp
				165					170					175	
Val	Ala	Lys	Pro	Val	Ile	Glu	Leu	Tyr	Lys	Ser	Arg	Gly	Val	Leu	His
			180					185					190		
Gln	Phe	Ser	Gly	Thr	Glu	Thr	Asn	Lys	Ile	Trp	Pro	Tyr	Val	Tyr	Thr
		195					200					205			
Leu	Phe	Ser	Asn	Lys	Ile	Thr	Pro	Ile	Gln	Ser	Lys	Glu	Ala	Tyr	
	210					215					220				